Phyre^2

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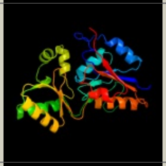
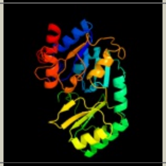
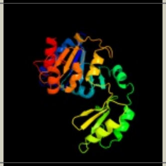
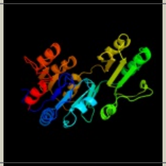
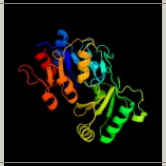
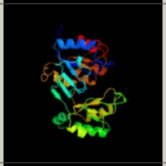
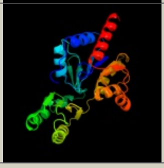
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1xvia_	Alignment		100.0	100	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
2	c1xviA_	Alignment		100.0	100	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative mannosyl-3-phosphoglycerate phosphatase; **PDBTitle:** crystal structure of yedp, phosphatase-like domain protein2 from escherichia coli k12
3	c3dnpA_	Alignment		100.0	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**stress response protein yhax; **PDBTitle:** crystal structure of stress response protein yhax from bacillus2 subtilis
4	c3niwA_	Alignment		100.0	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**haloacid dehalogenase-like hydrolase; **PDBTitle:** crystal structure of a haloacid dehalogenase-like hydrolase from2 bacteroides thetaiotaomicron
5	c3pgvB_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**haloacid dehalogenase-like hydrolase; **PDBTitle:** crystal structure of a haloacid dehalogenase-like hydrolase2 (kpn_04322) from klebsiella pneumoniae subsp. pneumoniae mgh 78578 at3 2.39 a resolution
6	d1nrwa_	Alignment		100.0	19	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
7	c3gygA_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ntd biosynthesis operon putative hydrolase ntdb; **PDBTitle:** crystal structure of yhjk (haloacid dehalogenase-like hydrolase2 protein) from bacillus subtilis
8	c3fzqA_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative hydrolase; **PDBTitle:** crystal structure of putative haloacid dehalogenase-like hydrolase2 (yp_001086940.1) from clostridium difficile 630 at 2.10 a resolution
9	c2qyhD_	Alignment		100.0	19	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical conserved protein, gk1056; **PDBTitle:** crystal structure of the hypothetical protein (gk1056) from2 geobacillus kaustophilus hta426
10	d1nf2a_	Alignment		100.0	18	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
11	d1rlma_	Alignment		100.0	15	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof

12	d2rbka1	Alignment		100.0	16	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
13	d1s2oa1	Alignment		100.0	22	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
14	c3daoB_	Alignment		100.0	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative phosphatse; **PDBTitle:** crystal structure of a putative phosphatse (eubrec_1417) from2 eubacterium rectale at 1.80 a resolution
15	d2b30a1	Alignment		100.0	15	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
16	d1rkqa_	Alignment		100.0	18	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
17	c3r4cA_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase, haloacid dehalogenase-like hydrolase; **PDBTitle:** divergence of structure and function among phosphatases of the2 haloalkanoate (had) enzyme superfamily: analysis of bt1666 from3 bacteroides thetaiotaomicron
18	c3l7yA_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein smu.1108c; **PDBTitle:** the crystal structure of smu.1108c from streptococcus mutans ua159
19	c3mpoD_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**predicted hydrolase of the had superfamily; **PDBTitle:** the crystal structure of a hydrolase from lactobacillus brevis
20	d1u02a_	Alignment		100.0	16	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Trehalose-phosphatase
21	d1wzca1	Alignment	not modelled	100.0	26	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
22	c2i55C_	Alignment	not modelled	100.0	12	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphomannomutase; **PDBTitle:** complex of glucose-1,6-bisphosphate with phosphomannomutase from2 leishmania mexicana
23	d1wr8a_	Alignment	not modelled	100.0	20	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
24	d2amya1	Alignment	not modelled	100.0	11	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
25	d1l6ra_	Alignment	not modelled	100.0	18	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
26	d2fuea1	Alignment	not modelled	100.0	14	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
27	d1k1ea_	Alignment	not modelled	99.9	30	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Probable phosphatase YrbI
28	c3e8mD_	Alignment	not modelled	99.9	23	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acylneuraminate cytidylyltransferase; **PDBTitle:** structure-function analysis of 2-keto-3-deoxy-d-glycero-d-galacto-2 nononate-9-phosphate (kdn) phosphatase defines a new clad within the3 type c0 had subfamily
						PDB header:hydrolase

29	c3mmzA_	Alignment	not modelled	99.9	26	**Chain:** A: **PDB Molecule:**putative had family hydrolase; **PDBTitle:** crystal structure of putative had family hydrolase from streptomyces2 avermitilis ma-4680
30	c3ewiB_	Alignment	not modelled	99.9	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**n-acylneuraminate cytidylyltransferase; **PDBTitle:** structural analysis of the c-terminal domain of murine cmp-2 sialic acid synthetase
31	c3mn1B_	Alignment	not modelled	99.9	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable yrbi family phosphatase; **PDBTitle:** crystal structure of probable yrbi family phosphatase from pseudomonas2 syringae pv.phaseolica 1448a
32	c2r8zC_	Alignment	not modelled	99.9	27	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**3-deoxy-d-manno-octulosonate 8-phosphate phosphatase; **PDBTitle:** crystal structure of yrbi phosphatase from escherichia coli in complex2 with a phosphate and a calcium ion
33	c2p9jH_	Alignment	not modelled	99.9	23	**PDB header:**structural genomics, unknown function **Chain:** H: **PDB Molecule:**hypothetical protein aq2171; **PDBTitle:** crystal structure of aq2171 from aquifex aeolicus
34	c3n1uA_	Alignment	not modelled	99.9	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase, had superfamily, subfamily iii a; **PDBTitle:** structure of putative had superfamily (subfamily iii a) hydrolase from2 legionella pneumophila
35	c3n07B_	Alignment	not modelled	99.9	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**3-deoxy-d-manno-octulosonate 8-phosphate phosphatase; **PDBTitle:** structure of putative 3-deoxy-d-manno-octulosonate 8-phosphate2 phosphatase from vibrio cholerae
36	c3n28A_	Alignment	not modelled	99.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphoserine phosphatase; **PDBTitle:** crystal structure of probable phosphoserine phosphatase from vibrio2 cholerae, unliganded form
37	c3fvvA_	Alignment	not modelled	99.8	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of the protein with unknown function from2 bordetella pertussis tohama i
38	c2hx1D_	Alignment	not modelled	99.8	10	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**predicted sugar phosphatases of the had **PDBTitle:** crystal structure of possible sugar phosphatase, had2 superfamily (zp_00311070.1) from cytophaga hutchinsonii3 atcc 33406 at 2.10 a resolution
39	c3p96A_	Alignment	not modelled	99.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphoserine phosphatase serb; **PDBTitle:** crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
40	c2cftA_	Alignment	not modelled	99.8	15	**PDB header:**phosphatase **Chain:** A: **PDB Molecule:**pyridoxal phosphate phosphatase; **PDBTitle:** crystal structure of human pyridoxal 5'-phosphate2 phosphatase with its substrate
41	d1j97a_	Alignment	not modelled	99.7	15	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Phosphoserine phosphatase
42	d1yv9a1	Alignment	not modelled	99.7	14	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**NagD-like
43	d1rkua_	Alignment	not modelled	99.7	12	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Homoserine kinase ThrH
44	d1wvia_	Alignment	not modelled	99.7	16	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**NagD-like
45	d1ydfa1	Alignment	not modelled	99.7	13	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**NagD-like
46	c3pdwA_	Alignment	not modelled	99.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized hydrolase yutf; **PDBTitle:** crystal structure of putative p-nitrophenyl phosphatase from bacillus2 subtilis
47	d1ys9a1	Alignment	not modelled	99.6	16	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**NagD-like
48	c3m1yA_	Alignment	not modelled	99.6	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphoserine phosphatase (serb); **PDBTitle:** crystal structure of a phosphoserine phosphatase (serb) from2 helicobacter pylori
49	c3kd3A_	Alignment	not modelled	99.5	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**phosphoserine phosphohydrolase-like protein; **PDBTitle:** crystal structure of a phosphoserine phosphohydrolase-like protein2 from francisella tularensis subsp. tularensis schu s4
50	d1nnla_	Alignment	not modelled	99.5	20	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Phosphoserine phosphatase
51	d1y8aa1	Alignment	not modelled	99.5	17	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**AF1437-like
52	c1zjjA_	Alignment	not modelled	99.5	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical protein ph1952; **PDBTitle:** crystal structure of hypothetical protein ph1952 from pyrococcus2 horikoshii ot3
53	d2c4na1	Alignment	not modelled	99.4	13	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**NagD-like
54	d1vjra_	Alignment	not modelled	99.4	17	**Fold:**HAD-like **Superfamily:**HAD-like

						Family: NagD-like
55	c3qgmC_	Alignment	not modelled	99.3	12	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**p-nitrophenyl phosphatase (pho2); **PDBTitle:** p-nitrophenyl phosphatase from archaeoglobus fulgidus
56	d2feaa1	Alignment	not modelled	99.3	16	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**MtnX-like
57	c2iyeC_	Alignment	not modelled	99.2	23	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**copper-transporting atpase; **PDBTitle:** structure of catalytic cpx-atpase domain copb-b
58	d1wpga2	Alignment	not modelled	99.2	18	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Meta-cation ATPase, catalytic domain P
59	d1zs9a1	Alignment	not modelled	98.9	11	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Enolase-phosphatase E1
60	d1u7pa_	Alignment	not modelled	98.9	21	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Magnesium-dependent phosphatase-1, Mdp1
61	c3b9bA_	Alignment	not modelled	98.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** structure of the e2 beryllium fluoride complex of the serca2 ca2+-atpase
62	c3l8hC_	Alignment	not modelled	98.9	20	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**putative haloacid dehalogenase-like hydrolase; **PDBTitle:** crystal structure of d,d-heptose 1.7-bisphosphate phosphatase from b.2 bronchiseptica complexed with magnesium and phosphate
63	c3rfuC_	Alignment	not modelled	98.9	20	**PDB header:**hydrolase, membrane protein **Chain:** C: **PDB Molecule:**copper efflux atpase; **PDBTitle:** crystal structure of a copper-transporting pib-type atpase
64	d2hcfa1	Alignment	not modelled	98.8	17	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**beta-Phosphoglucomutase-like
65	d2b8ea1	Alignment	not modelled	98.7	35	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Meta-cation ATPase, catalytic domain P
66	c1mhsA_	Alignment	not modelled	98.7	21	**PDB header:**membrane protein, proton transport **Chain:** A: **PDB Molecule:**plasma membrane atpase; **PDBTitle:** model of neurospora crassa proton atpase
67	c2zxeA_	Alignment	not modelled	98.7	18	**PDB header:**hydrolase/transport protein **Chain:** A: **PDB Molecule:**na, k-atpase alpha subunit; **PDBTitle:** crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
68	c3j08A_	Alignment	not modelled	98.7	30	**PDB header:**hydrolase, metal transport **Chain:** A: **PDB Molecule:**copper-exporting p-type atpase a; **PDBTitle:** high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
69	d1cr6a1	Alignment	not modelled	98.6	22	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**YihX-like
70	c3j09A_	Alignment	not modelled	98.6	30	**PDB header:**hydrolase, metal transport **Chain:** A: **PDB Molecule:**copper-exporting p-type atpase a; **PDBTitle:** high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
71	c2ho4A_	Alignment	not modelled	98.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**haloacid dehalogenase-like hydrolase domain **PDBTitle:** crystal structure of protein from mouse mm.236127
72	d1xpja_	Alignment	not modelled	98.6	14	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Hypothetical protein VC0232
73	c3ixzA_	Alignment	not modelled	98.6	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**potassium-transporting atpase alpha; **PDBTitle:** pig gastric h+/k+-atpase complexed with aluminium fluoride
74	d2o2xa1	Alignment	not modelled	98.6	18	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Histidinol phosphatase-like
75	c3kzxA_	Alignment	not modelled	98.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**had-superfamily hydrolase, subfamily ia, variant 1; **PDBTitle:** crystal structure of a had-superfamily hydrolase from ehrlichia2 chaffeensis at 1.9a resolution
76	c3b8cB_	Alignment	not modelled	98.6	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atpase 2, plasma membrane-type; **PDBTitle:** crystal structure of a plasma membrane proton pump
77	c3iruA_	Alignment	not modelled	98.6	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phoshonoacetaldehyde hydrolase like protein; **PDBTitle:** crystal structure of phoshonoacetaldehyde hydrolase like protein from2 oleispira antarctica
78	c2pibA_	Alignment	not modelled	98.5	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphorylated carbohydrates phosphatase tm_1254; **PDBTitle:** crystal structure of putative beta-phosphoglucomutase from2 thermotoga maritima
79	c3m9lA_	Alignment	not modelled	98.5	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase, haloacid dehalogenase-like family; **PDBTitle:** crystal structure of probable had family hydrolase from2

						pseudomonas fluorescens pf-5
80	c3d6jA_	Alignment	not modelled	98.5	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative haloacid dehalogenase-like hydrolase; **PDBTitle:** crystal structure of putative haloacid dehalogenase-like hydrolase2 from bacteroides fragilis
81	c3mc1A_	Alignment	not modelled	98.5	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**predicted phosphatase, had family; **PDBTitle:** crystal structure of a predicted phosphatase from2 clostridium acetobutylicum
82	d2hsza1	Alignment	not modelled	98.5	24	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**beta-Phosphoglucomutase-like
83	d2gmwa1	Alignment	not modelled	98.5	15	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Histidinol phosphatase-like
84	c1cr6A_	Alignment	not modelled	98.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**epoxide hydrolase; **PDBTitle:** crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
85	c2hi0B_	Alignment	not modelled	98.4	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative phosphoglycolate phosphatase; **PDBTitle:** crystal structure of putative phosphoglycolate phosphatase2 (yp_619066.1) from lactobacillus delbrueckii subsp. bulgaricus atcc3 baa-365 at 1.51 a resolution
86	d2obba1	Alignment	not modelled	98.4	20	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**BT0820-like
87	c3esqA_	Alignment	not modelled	98.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**d,d-heptose 1,7-bisphosphate phosphatase; **PDBTitle:** crystal structure of calcium-bound d,d-heptose 1.7-2 bisphosphate phosphatase from e. coli
88	c3b8eC_	Alignment	not modelled	98.4	14	**PDB header:**hydrolase/transport protein **Chain:** C: **PDB Molecule:**sodium/potassium-transporting atpase subunit **PDBTitle:** crystal structure of the sodium-potassium pump
89	c3s6jC_	Alignment	not modelled	98.3	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**hydrolase, haloacid dehalogenase-like family; **PDBTitle:** the crystal structure of a hydrolase from pseudomonas syringae
90	d2fpwa1	Alignment	not modelled	98.3	18	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Histidinol phosphatase-like
91	d1ltqa1	Alignment	not modelled	98.2	17	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**phosphatase domain of polynucleotide kinase
92	d2gfha1	Alignment	not modelled	98.2	12	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**beta-Phosphoglucomutase-like
93	d2ah5a1	Alignment	not modelled	98.2	14	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**beta-Phosphoglucomutase-like
94	d1zd3a1	Alignment	not modelled	98.2	15	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**YihX-like
95	c2b8eB_	Alignment	not modelled	98.2	24	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**cation-transporting atpase; **PDBTitle:** copa atp binding domain
96	d1swva_	Alignment	not modelled	98.2	16	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Phosphonoacetaldehyde hydrolase-like
97	d2vkqa1	Alignment	not modelled	98.2	13	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Pyrimidine 5'-nucleotidase (UMPH-1)
98	c3dv9A_	Alignment	not modelled	98.2	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**beta-phosphoglucomutase; **PDBTitle:** putative beta-phosphoglucomutase from bacteroides vulgatus.
99	d2fdra1	Alignment	not modelled	98.1	10	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**beta-Phosphoglucomutase-like
100	c2om6A_	Alignment	not modelled	98.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable phosphoserine phosphatase; **PDBTitle:** hypothetical protein (probable phosphoserine phosph (ph0253) from2 pyrococcus horikoshii ot3
101	d1o08a_	Alignment	not modelled	98.0	12	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**beta-Phosphoglucomutase-like
102	c3cnhA_	Alignment	not modelled	98.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase family protein; **PDBTitle:** crystal structure of predicted hydrolase of haloacid dehalogenase-like2 superfamily (np_295428.1) from deinococcus radiodurans at 1.66 a3 resolution
103	c3nuqA_	Alignment	not modelled	98.0	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative nucleotide phosphatase; **PDBTitle:** structure of a putative nucleotide phosphatase from saccharomyces2 cerevisiae
104	d2go7a1	Alignment	not modelled	97.9	13	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**beta-Phosphoglucomutase-like
						PDB header:hydrolase

105	c3sd7A_	Alignment	not modelled	97.9	19	**Chain:** A: **PDB Molecule:**putative phosphatase; **PDBTitle:** 1.7 angstrom resolution crystal structure of putative phosphatase from2 clostridium difficile
106	d1te2a_	Alignment	not modelled	97.9	15	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**beta-Phosphoglucomutase-like
107	c3ib6B_	Alignment	not modelled	97.9	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from listeria2 monocytogenes serotype 4b
108	d1zrna_	Alignment	not modelled	97.8	19	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**HAD-related
109	c2pkeA_	Alignment	not modelled	97.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**haloacid delahogenase-like family hydrolase; **PDBTitle:** crystal structure of haloacid delahogenase-like family hydrolase2 (np_639141.1) from xanthomonas campestris at 1.81 a resolution
110	d1x42a1	Alignment	not modelled	97.8	10	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**HAD-related
111	c2w11B_	Alignment	not modelled	97.8	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**2-haloalkanoic acid dehalogenase; **PDBTitle:** structure of the l-2-haloacid dehalogenase from sulfolobus2 tokodaii
112	c3l5kA_	Alignment	not modelled	97.8	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**haloacid dehalogenase-like hydrolase domain- **PDBTitle:** the crystal structure of human haloacid dehalogenase-like2 hydrolase domain containing 1a (hdhd1a)
113	d1qq5a_	Alignment	not modelled	97.7	14	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**HAD-related
114	c2hoqA_	Alignment	not modelled	97.7	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative had-hydrolase ph1655; **PDBTitle:** crystal structure of the probable haloacid dehalogenase (ph1655) from2 pyrococcus horikoshii ot3
115	c2ia5C_	Alignment	not modelled	97.7	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**polynucleotide kinase; **PDBTitle:** t4 polynucleotide kinase/phosphatase with bound sulfate and2 magnesium.
116	d2fi1a1	Alignment	not modelled	97.7	14	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Phosphonoacetaldehyde hydrolase-like
117	c2yy6B_	Alignment	not modelled	97.6	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**phosphoglycolate phosphatase; **PDBTitle:** crystal structure of the phosphoglycolate phosphatase from aquifex2 aeolicus vf5
118	c2qltA_	Alignment	not modelled	97.6	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**(dl)-glycerol-3-phosphatase 1; **PDBTitle:** crystal structure of an isoform of dl-glycerol-3-phosphatase, rhr2p,2 from saccharomyces cerevisiae
119	c3qnmA_	Alignment	not modelled	97.6	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**haloacid dehalogenase-like hydrolase; **PDBTitle:** haloalkane dehalogenase family member from bacteroides2 thetaiotaomicron of unknown function
120	c3e58A_	Alignment	not modelled	97.6	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative beta-phosphoglucomutase; **PDBTitle:** crystal structure of putative beta-phosphoglucomutase from2 streptococcus thermophilus